SEQUENCE LISTING

<110> Beals, John

       Kuchibhotla, Uma

<120> HETEROLOGOUS G-CSF FUSION PROTEINS

<130> P-15648

<160> 66

<170> PatentIn version 3.1

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<223> Xaa at position 38 is Thr, or any other amino acid exept Pro;

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<222> (39)..(39)

<223> Xaa at position 39 is Tyr, Thr, or Ser;

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<222> (57)..(57)

<223> Xaa at position 57 is Pro or Val;

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<223> Xaa at position 58 is Trp or Asn;

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<223> Xaa at position 61 is Leu, or any other amino acid except Pro;

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<222> (62)..(62)

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<223> Xaa at position 63 Ser or Asn;

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<222> (66)..(66)

<223> Xaa at position 66 is Ser or Thr;

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<222> (67)..(67)

<223> Xaa at position 67 is Gln or Asn;

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<223> Xaa at position 93 is Glu or Asn;

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<223> Xaa at position 133 is Thr or Asn;

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<223> Xaa at position 134 is Gln or any other amino acid except Pro;

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<222> (135)..(135)

<223> Xaa at position 135 is Gly, Ser, or Thr;

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<222> (141)..(141)

<223> Xaa at position 141 is Ala or Asn;

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<222> (142)..(142)

<223> Xaa at position 142 is Ser or any other amino acid except Pro;

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Glu Lys Leu Cys Xaa Xaa Xaa Lys Leu Cys His Pro Glu Glu Leu Val
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Leu Leu Gly His Ser Leu Gly Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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Xaa Xaa Xaa Xaa Xaa Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
65                  70                  75                  80


Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Xaa Xaa Xaa Ser
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Xaa Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
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cagggcgatg gcgcagcgct ccagcggaat ctcgttcact ccttctaggt cccgctaccg     180

cgtcgcgagg tcgagaagct gtgtaacacc accaagctgt gccaccccga ggagctggtg     240

ctcttcgaca cattgtggtg gttcgacacg gtggggctcc tcgaccacct gctcggacac     300

tctctgggca tcccctgggc tcccctgagc agctgcgacg agcctgtgac agacccgtag     360

gggacccgag gggactcgtc gacgcccagc caggccctgc agctggcagg ctgcttgagc     420

caactccata gcgggtcggt ccgggacgtc gaccgtccga cgaactcggt tgaggtatcg     480

ggccttttcc tctaccaggg gctcctgcag gccctggaag ggatctcccc ggaaaaggag     540

atggtccccg aggacgtccg ggaccttccc tagaggcccg agttgggtcc caccttggac     600

acactgcagc tggacgtcgc cgacgggctc aacccagggt ggaacctgtg tgacgtcgac     660

ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggcccct     720

aaacggtggt ggtagaccgt cgtctacctt cttgaccctt accggggagc cctgcagccc     780

acccagggtg ccatgccggc cttcaactct accttccggg acgtcgggtg ggtcccacgg     840

tacggccgga agttgagatg gaagcagcgc cgggcaggag gggtcctggt tgcctcccat     900

ctgcagagct tcgtcgcggc ccgtcctccc caggaccaac ggagggtaga cgtctcgaag     960
```

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ctggaggtgt cgtaccgcgt cttaaggcac cttgcccagc ccgacctcca cagcatggcg      1020

cagaattccg tggaacgggt cggg                                            1044


<210>   12

<211>   1044

<212>   DNA

<213>   Artificial Sequence


<220>

<223>   synthetic construct

<400>   12
acccccctgg gccctgccag ctccctgccc cagagcttcc tgctcaagtg gggggacccg       60

ggacggtcga gggacggggt ctcgaaggac gagttcgcct tagagcaagt gaggaagatc      120

cagggcgatg cgcagcgct ccagcggaat ctcgttcact ccttctaggt cccgctaccg       180

cgtcgcgagg tcgagaagct gtgtaacacc accaagctgt gccaccccga ggagctggtg      240

ctcttcgaca cattgtggtg gttcgacacg gtggggctcc tcgaccacct gctcggacac      300

tctctgggca tcgttaacgc taccctgagc agctgcgacg agcctgtgac agacccgtag      360

caattgcgat gggactcgtc gacgcccagc caggccctgc agctggcagg ctgcttgagc      420

caactccata gcgggtcggt ccgggacgtc gaccgtccga cgaactcggt tgaggtatcg      480

ggccttttcc tctaccaggg gctcctgcag gccctggaag ggatctcccc ggaaaaggag      540

atggtccccg aggacgtccg ggaccttccc tagaggcccg agttgggtcc caccttggac      600

acactgcagc tggacgtcgc cgacgggctc aacccagggt ggaacctgtg tgacgtcgac      660

ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggcccct      720

aaacggtggt ggtagaccgt cgtctacctt cttgaccctt accggggagc cctgcagccc      780

acccagggtg ccatgccggc cttcgcctct gctttccggg acgtcgggtg ggtcccacgg      840

tacggccgga agcggagacg aaagcagcgc cgggcaggag gggtcctggt tgcctcccat      900

ctgcagagct tcgtcgcggc ccgtcctccc caggaccaac ggagggtaga cgtctcgaag      960

ctggaggtgt cgtaccgcgt cttaaggcac cttgcccagc ccgacctcca cagcatggcg     1020

cagaattccg tggaacgggt cggg                                           1044
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<210> 13

<211> 1044

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 13
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acccccctgg gccctgccag ctccctgccc cagagcttcc tgctcaagtg gggggacccg        60

ggacggtcga gggacggggt ctcgaaggac gagttcgcct tagagcaagt gaggaagatc       120

cagggcgatg cgcagcgct  ccagcggaat ctcgttcact ccttctaggt cccgctaccg       180

cgtcgcgagg tcgagaagct gtgtaacacc accaagctgt gccaccccga ggagctggtg       240

ctcttcgaca cattgtggtg gttcgacacg gtggggctcc tcgaccacct gctcggacac       300

tctctgggca tcccctgggc tcccctgagc agctgcgacg agcctgtgac agacccgtag       360

gggacccgag gggactcgtc gacgcccagc aacgccaccc agctggcagg ctgcttgagc       420

caactccata gcgggtcgtt gcggtgggtc gaccgtccga cgaactcggt tgaggtatcg       480

ggccttttcc tctaccaggg gctcctgcag gccctggaag ggatctcccc ggaaaaggag       540

atggtccccg aggacgtccg ggaccttccc tagaggcccg agttgggtcc caccttggac       600

acactgcagc tggacgtcgc cgacgggctc aacccagggt ggaacctgtg tgacgtcgac       660

ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggcccct       720

aaacggtggt ggtagaccgt cgtctacctt cttgaccctt accggggagc cctgcagccc       780

acccagggtg ccatgccggc cttcgcctct gctttccggg acgtcgggtg ggtcccacgg       840

tacggccgga agcggagacg aaagcagcgc cgggcaggag gggtcctggt tgcctcccat       900

ctgcagagct tcgtcgcggc ccgtcctccc caggaccaac ggagggtaga cgtctcgaag       960

ctggaggtgt cgtaccgcgt cttaaggcac cttgcccagc ccgacctcca cagcatggcg      1020

cagaattccg tggaacgggt cggg                                             1044
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<210> 14

<211> 1044

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 14

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acccccctgg gccctgccag ctccctgccc cagagcttcc tgctcaagtg gggggacccg        60

ggacggtcga gggacggggt ctcgaaggac gagttcgcct tagagcaagt gaggaagatc       120

cagggcgatg gcgcagcgct ccagcggaat ctcgttcact ccttctaggt cccgctaccg       180

cgtcgcgagg tcgagaagct gtgtaacacc accaagctgt gccaccccga ggagctggtg       240

ctcttcgaca cattgtggtg gttcgacacg gtggggctcc tcgaccacct gctcggacac       300

tctctgggca tcccctgggc tcccctgagc agctgcgacg agcctgtgac agacccgtag       360

gggacccgag gggactcgtc gacgcccagc caggccctgc agctggcagg ctgcttgagc       420

caactccata gcgggtcggt ccgggacgtc gaccgtccga cgaactcggt tgaggtatcg       480

ggccttttcc tctaccaggg gctcctgcag gccctggaag ggatctcccc ggaaaaggag       540

atggtccccg aggacgtccg ggaccttccc tagaggaacg gtaccggtcc caccttggac       600

acactgcagc tggacgtcgc cgacttgcca tggccagggt ggaacctgtg tgacgtcgac       660

ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggcccct       720

aaacggtggt ggtagaccgt cgtctacctt cttgaccctt accggggagc cctgcagccc       780

acccagggtg ccatgccggc cttcgcctct gctttccggg acgtcgggtg ggtcccacgg       840

tacggccgga agcggagacg aaagcagcgc cgggcaggag gggtcctggt tgcctcccat       900

ctgcagagct tcgtcgcggc ccgtcctccc caggaccaac ggagggtaga cgtctcgaag       960

ctggaggtgt cgtaccgcgt cttaaggcac cttgcccagc ccgacctcca cagcatggcg      1020

cagaattccg tggaacgggt cggg                                            1044
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<210> 15

<211> 1044

<212> DNA

<213> Artificial Sequence

<220>

<223>   synthetic construct

<400>   15
acccccctgg gccctgccag ctccctgccc cagagcttcc tgctcaagtg gggggacccg   60

ggacggtcga gggacggggt ctcgaaggac gagttcgcct tagagcaagt gaggaagatc   120

cagggcgatg gcgcagcgct ccagcggaat ctcgttcact ccttctaggt cccgctaccg   180

cgtcgcgagg tcgagaagct gtgtaacacc accaagctgt gccaccccga ggagctggtg   240

ctcttcgaca cattgtggtg gttcgacacg gtggggctcc tcgaccacct gctcggacac   300

tctctgggca tcgttaacgc taccctgagc agctgcgacg agcctgtgac agacccgtag   360

caattgcgat gggactcgtc gacgcccagc aacgccaccc agctggcagg ctgcttgagc   420

caactccata gcgggtcgtt gcggtgggtc gaccgtccga cgaactcggt tgaggtatcg   480

ggccttttcc tctaccaggg gctcctgcag gccctggaag ggatctcccc ggaaaaggag   540

atggtccccg aggacgtccg ggaccttccc tagaggcccg agttgggtcc caccttggac   600

acactgcagc tggacgtcgc cgacgggctc aacccagggt ggaacctgtg tgacgtcgac   660

ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggcccct   720

aaacggtggt ggtagaccgt cgtctacctt cttgaccctt accggggagc cctgcagccc   780

acccagggtg ccatgccggc cttcgcctct gctttccggg acgtcgggtg ggtcccacgg   840

tacggccgga agcggagacg aaagcagcgc cgggcaggag gggtcctggt tgcctcccat   900

ctgcagagct tcgtcgcggc ccgtcctccc caggaccaac ggagggtaga cgtctcgaag   960

ctggaggtgt cgtaccgcgt cttaaggcac cttgcccagc ccgacctcca cagcatggcg   1020

cagaattccg tggaacgggt cggg   1044

<210>   16

<211>   1044

<212>   DNA

<213>   Artificial Sequence

<220>

<223>   synthetic construct

<400>   16
acccccctgg gccctgccag ctccctgccc cagagcttcc tgctcaagtg gggggacccg   60

ggacggtcga gggacggggt ctcgaaggac gagttcgcct tagagcaagt gaggaagatc   120

```
cagggcgatg gcgcagcgct ccagcggaat ctcgttcact ccttctaggt cccgctaccg      180

cgtcgcgagg tcgagaagct gtgtaacacc accaagctgt gccaccccga ggagctggtg      240

ctcttcgaca cattgtggtg gttcgacacg gtggggctcc tcgaccacct gctcggacac      300

tctctgggca tcccctgggc tcccctgagc aattgcgacg agcctgtgac agacccgtag      360

gggacccgag gggactcgtt aacgaccagc caggccctgc agctggcagg ctgcttgagc      420

caactccata gctggtcggt ccgggacgtc gaccgtccga cgaactcggt tgaggtatcg      480

ggccttttcc tctaccaggg gctcctgcag gccctgaacg ggacctcccc ggaaaaggag      540

atggtccccg aggacgtccg ggacttgccc tggaggcccg agttgggtcc caccttggac      600

acactgcagc tggacgtcgc cgacgggctc aacccagggt ggaacctgtg tgacgtcgac      660

ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggcccct      720

aaacggtggt ggtagaccgt cgtctacctt cttgaccctt accggggagc cctgcagccc      780

acccagggtg ccatgccggc cttcgcctct gctttccggg acgtcgggtg ggtcccacgg      840

tacggccgga agcggagacg aaagcagcgc cgggcaggag gggtcctggt tgcctcccat      900

ctgcagagct tcgtcgcggc ccgtcctccc caggaccaac ggagggtaga cgtctcgaag      960

ctggaggtgt cgtaccgcgt cttaaggcac cttgcccagc ccgacctcca cagcatggcg     1020

cagaattccg tggaacgggt cggg                                             1044
```

<210> 17

<211> 1762

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 17
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gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta      120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa      180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt      240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa      300
```

```
tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt      360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat      420

gaaattgcca gaagacatcc ttactttat gccccggaac tccttttctt tgctaaaagg       480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca      540

aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt      600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc      660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa      720

gtccacacgg aatgctgcca tggagatctg cttgaatgtg ctgatgacag ggcggacctt      780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa      840

aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct      900

gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct      960

gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcatcctgat     1020

tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc     1080

tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt     1140

gtggaagagc ctcagaattt aatcaaacaa aattgtgagc tttttgagca gcttggagag     1200

tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtacccca agtgtcaact     1260

ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gcagcaaatg ttgtaaacat     1320

cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta     1380

tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc     1440

ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg atgaaacata cgttcccaaa     1500

gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag     1560

agacaaatca gaaacaaac tgcacttgtt gagctcgtga acacaagcc caaggcaaca      1620

aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag     1680

gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa     1740

gctgccttag gcttataatg ac                                             1762
```

<210> 18

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 18

```
Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1               5                   10                  15

Ala Pro Glu Lys Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Lys Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190
```

```
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195             200             205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210             215             220

Ser Leu Ser Leu Ser Pro Gly Lys
225             230
```

<210> 19

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic contruct

<400> 19

```
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1           5               10              15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
            20              25              30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
        35              40              45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
    50              55              60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65              70              75              80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
            85              90              95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
            100             105             110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
        115             120             125
```

```
Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
    130                 135             140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145                 150             155                 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
                165             170             175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
            180             185             190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
        195             200             205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
    210             215             220

Leu Ser Leu Gly Lys
225
```

```
<210>  20

<211>  585

<212>  PRT

<213>  Artificial Sequence


<220>

<223>  synthetic construct

<400>  20
```

```
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1               5               10              15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20              25              30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
        35              40              45
```

```
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50              55              60


Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65              70              75              80


Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
            85              90              95


Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100             105             110


Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115             120             125


Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130             135             140


Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145             150             155             160


Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
            165             170             175


Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
        180             185             190


Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195             200             205


Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
    210             215             220


Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225             230             235             240


Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
            245             250             255


Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
        260             265             270


Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
    275             280             285
```

```
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290              295              300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305              310              315                  320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
            325              330                  335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340              345              350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355              360              365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370              375              380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Asn Leu Gly Glu
385              390              395              400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
            405              410              415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420              425              430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435              440              445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450              455              460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465              470              475              480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
            485              490              495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500              505              510
```

```
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525


Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540


Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560


Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575


Ala Ala Ser Gln Ala Ala Leu Gly Leu
            580                 585
```

<210> 21

<211> 703

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

```
<400> 21
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gggggaccgt cagtcttcct cttccccca aaacccaagg acaccctcat gatctcccgg    120

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc    180

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag    240

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat    300

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc    360

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg    420

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc    480

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct    540

cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc    600

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac    660

tacacgcaga agagcctctc cctgtctccg ggtaaatgat agt                       703
```

```
<210>  22

<211>  981

<212>  DNA

<213>  Artificial Sequence


<220>

<223>  synthetic construct

<400>  22
tccaccaagg gcccatcggt cttcccgcta gcgccctgct ccaggagcac ctccgagagc      60

acagccgccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg     120

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga     180

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac gaagacctac     240

acctgcaacg tagatcacaa gcccagcaac accaaggtgg acaagagagt tgagtccaaa     300

tatggtcccc catgcccacc ctgcccagca cctgagttcc tggggggacc atcagtcttc     360

ctgttccccc caaaacccaa ggacactctc atgatctccc ggacccctga ggtcacgtgc     420

gtggtggtgg acgtgagcca ggaagacccc gaggtccagt tcaactggta cgtggatggc     480

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agttcaacag cacgtaccgt     540

gtggtcagcg tcctcaccgt cctgcaccag gactggctga acggcaagga gtacaagtgc     600

aaggtctcca acaaaggcct cccgtcctcc atcgagaaaa ccatctccaa agccaaaggg     660

cagccccgag agccacaggt gtacaccctg cccccatccc aggaggagat gaccaagaac     720

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg     780

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac     840

ggctccttct tcctctacag caggctaacc gtggacaaga gcaggtggca ggaggggaat     900

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagagcctc     960

tccctgtctc tgggtaaatg a                                              981


<210>  23

<211>  406

<212>  PRT
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<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 23

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
1   5   10   15

Ala Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
            20   25   30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
        35   40   45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
    50   55   60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
65   70   75   80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
                85   90   95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
            100   105   110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
        115   120   125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
    130   135   140

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
145   150   155   160

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Glu Pro
                165   170   175

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                180   185   190

```
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        195             200             205

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    210             215             220

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
225             230             235             240

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
            245             250             255

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        260             265             270

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
        275             280             285

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
    290             295             300

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
305             310             315             320

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            325             330             335

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            340             345             350

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
    355             360             365

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    370             375             380

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
385             390             395             400

Ser Leu Ser Pro Gly Lys
            405
```

<210> 24

<211> 403

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 24

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Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
1               5                   10                  15


Ala Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
            20                  25                  30


Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
        35                  40                  45


Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
    50                  55                  60


Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
65                  70                  75                  80


Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
                85                  90                  95


Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
            100                 105                 110


Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
        115                 120                 125


Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
    130                 135                 140


Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
145                 150                 155                 160


Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Glu Ser
                165                 170                 175
```

```
Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly
            180         185             190

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            195             200             205

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln
    210             215             220

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
225             230             235             240

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr
            245             250             255

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            260             265             270

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile
        275             280             285

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
    290             295             300

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser
305             310             315             320

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
            325             330             335

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            340             345             350

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val
        355             360             365

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met
        370             375             380

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
385             390             395             400

Leu Gly Lys
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<210> 25

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 25

```
Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
1               5                   10                  15


Ala Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
            20                  25                  30


Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
            35                  40                  45


Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
        50                  55                  60


Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
.65                  70                  75                  80


Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
                85                  90                  95


Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
                100                 105                 110


Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
            115                 120                 125


Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
        130                 135                 140


Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
145                 150                 155                 160
```

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Gly Gly
                165   170   175

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ala His
            180   185   190

Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe
        195   200   205

Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro
    210   215   220

Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys
225   230   235   240

Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His
            245   250   255

Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr
            260   265   270

Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn
        275   280   285

Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu
    290   295   300

Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu
305   310   315   320

Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro
            325   330   335

Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala
        340   345   350

Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu
        355   360   365

Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys
    370   375   380

Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe
385   390   395   400

Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu
        405   410   415

Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr
        420   425   430

Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp
        435   440   445

Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu
    450   455   460

Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala
465   470   475   480

Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala
        485   490   495

Asp Phe Val Glu
        500

<210>   26

<211>   69

<212>   DNA

<213>   Artificial Sequence

<220>

<223>   synthetic construct

<400>   26
gtaagcttgc gtcgacgcta gcggcgcgcc gccatggccg gacctgccac ccagagcccc   60

atgaagctg   69

<210>   27

<211>   61

<212>   DNA

<213>   Artificial Sequence

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<220>

<223>  synthetic construct

<400>  27
ggggcaggga gctggctggg cccagtggag tggcttcctg cactgtccag agtgcactgt      60

g                                                                     61



<210>  28

<211>  59

<212>  DNA

<213>  Artificial Sequence



<220>

<223>  synthetic construct

<400>  28
ggacagtgca ggaagccact ccactgggcc cagccagctc cctgccccag agcttcctg       59



<210>  29

<211>  72

<212>  DNA

<213>  Artificial Sequence



<220>

<223>  synthetic construct

<400>  29
gaacctcgag gatcctcatt agggctgggc aaggtgcctt aagacgcggt acgacacctc      60

caggaagctc tg                                                          72



<210>  30

<211>  69

<212>  DNA

<213>  Artificial Sequence
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<220>

<223> synthetic construct

<400> 30
gtaagcttgc gtcgacgcta gcggcgcgcc gccatggccg gacctgccac ccagagcccc   60

atgaagctg   69

<210> 31

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 31
gctctaaggc cttgagcagg aagctctggg gcagggagct cgctgggccc agtggag   57

<210> 32

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 32
gggcccagcg agctccctgc cccagagctt cctgctcaag gccttagagc aag   53

<210> 33

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 33
gaacctcgag gatcctcatt agggctgggc aaggtgcctt aagacgcggt acgacacctc   60

caggaagctc tg   72

<210> 34

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 34
gtaagcttgc gtcgacgcta gcggcgcgcc gccatggccg gacctgccac ccagagcccc   60

atgaagctg   69

<210> 35

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 35
gtccgagcag cactagttcc tcggggtggc acagcttggt ggtgttacac agcttctcct   60

g   61

<210> 36

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 36
ggcgcagcgc tccaggagaa gctgtgtaac accaccaagc tgtgccaccc cgaggaacta   60

gtgctg   66

<210> 37

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 37
gaacctcgag gatcctcatt agggctgggc aaggtgcctt aagacgcggt acgacacctc   60

caggaagctc tg   72

<210> 38

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 38
gtaagcttgc gtcgacgcta gcggcgcgcc gccatggccg gacctgccac ccagagcccc   60

atgaagctg   69

<210> 39

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 39
gcccggcgct ggaaagcgct ggcgaaggcc ggcatggcgg tctggttggg ctgcagggca   60

g   61

<210> 40

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 40
ggcccctgcc ctgcagccca accagaccgc catgccggcc ttcgccagcg ctttccagcg   60

<210> 41

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 41
gaacctcgag gatcctcatt agggctgggc aaggtgcctt aagacgcggt acgacacctc   60

caggaagctc tg   72

<210> 42

<211> 69

<212> DNA

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<213>  Artificial Sequence


<220>

<223>  synthetic construct

<400>  42
gtaagcttgc gtcgacgcta gcggcgcgcc gccatggccg gacctgccac ccagagcccc      60

atgaagctg                                                             69


<210>  43

<211>  68

<212>  DNA

<213>  Artificial Sequence


<220>

<223>  synthetic construct

<400>  43
gcccggcgct ggaaggtaga gttgaaggcc ggcatggcac cctgggtggg ctgaagagca      60

ggggccat                                                              68


<210>  44

<211>  74

<212>  DNA

<213>  Artificial Sequence


<220>

<223>  synthetic construct

<400>  44
gggaatggcc cctgctcttc agcccaccca gggtgccatg ccggccttca actctacctt      60

ccagcgccgg gcag                                                       74


<210>  45

<211>  72
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<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 45
gaacctcgag gatcctcatt agggctgggc aaggtgcctt aagacgcggt acgacacctc   60

caggaagctc tg   72

<210> 46

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 46
gctagcggcg cgccaccatg   20

<210> 47

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 47
gctcagggta gcgttaacga tgcccagaga gtg   33

<210> 48

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 48
gggcatcgtt aacgctaccc tgagcagctg   30

<210> 49

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 49
gactcgagga tcctcattag ggctggg   27

<210> 50

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 50
gctagcggcg cgccaccatg gccggacctg ccacccag   38

<210> 51

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 51
caagcagccg gccagctggg tggcgttgct ggggcagctg ctcag   45

<210> 52

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 52
gccccagcaa cgccacccag ctggccggct gcttgag   37

<210> 53

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 53
gactcgagga tcctcattag ggctgggcaa ggtgccttaa gacgcgg   47

<210> 54

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

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<400>  54
gctagcggcg cgccaccatg                                           20


<210>  55

<211>  27

<212>  DNA

<213>  Artificial Sequence



<220>

<223>  synthetic construct

<400>  55
ggggcaacta gtcaggttag cccaggg                                   27


<210>  56

<211>  27

<212>  DNA

<213>  Artificial Sequence



<220>

<223>  synthetic construct

<400>  56
gctaacctga ctagttgccc cagccag                                   27


<210>  57

<211>  27

<212>  DNA

<213>  Artificial Sequence



<220>

<223>  synthetic construct

<400>  57
gactcgagga tcctcattag ggctggg                                   27
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<210> 58

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 58
gctagcggcg cgccaccatg   20

<210> 59

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 59
ggtgcaattg ctcaggggag cccag   25

<210> 60

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 60
gcaattgcac cagccaggcc ctg   23

<210> 61

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 61
gactcgagga tcctcattag ggctggg   27

<210> 62

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 62
gctagcggcg cgccaccatg gccggacctg ccacccag   38

<210> 63

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 63
ccggactggt cccgttcagg gcctgcagga gcccctg   37

<210> 64

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 64
gaacgggacc agtccggagt tgggtcccac cttgg   35

<210> 65

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 65
gactcgagga tcctcattag ggctgggcaa ggtgccttaa gacgcgg   47

<210> 66

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 66
gtcgacgcta gcggcgcgcc accatggccg gacctg   36